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=====

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).  
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:  
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query length: 9 AA  
Date run: 2004-08-04 13:20:52 UTC+0100 on sib-gm1.unil.ch  
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]  
Database: EXPASY/UniProt  
1,529,856 sequences; 486,583,783 total letters

[Taxonomic view](#)

[NiceBlast view](#)

[Printable view](#)

#### List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

	Db	AC	Description	Score	E-value
<input type="checkbox"/>	tr	<a href="#">Q8NXX6</a>	Ser-Asp rich fibrinogen-binding bone sialoprotein-bind...	34	0.23
<input type="checkbox"/>	tr	<a href="#">Q8NXX5</a>	Ser-Asp rich fibrinogen-binding bone sialoprotein-bind...	34	0.23
<input type="checkbox"/>	tr	<a href="#">Q8CQ72</a>	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	34	0.23
<input type="checkbox"/>	tr	<a href="#">Q99W47</a>	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	34	0.23
<input type="checkbox"/>	tr	<a href="#">Q99W46</a>	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	34	0.23
<input type="checkbox"/>	tr	<a href="#">Q932F7</a>	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	34	0.23
<input type="checkbox"/>	tr	<a href="#">Q6GBS5</a>	Putative surface anchored protein [SAS0520] [Staphyloc...	34	0.23
<input type="checkbox"/>	tr	<a href="#">Q6GBS4</a>	Bone sialoprotein-binding protein [SAS0521] [Staphyloc...	34	0.23
<input type="checkbox"/>	tr	<a href="#">Q7A780</a>	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	34	0.23
<input type="checkbox"/>	tr	<a href="#">Q9KI13</a>	Fibrinogen-binding protein SdrG [sdrG] [Staphylococcus...	34	0.23

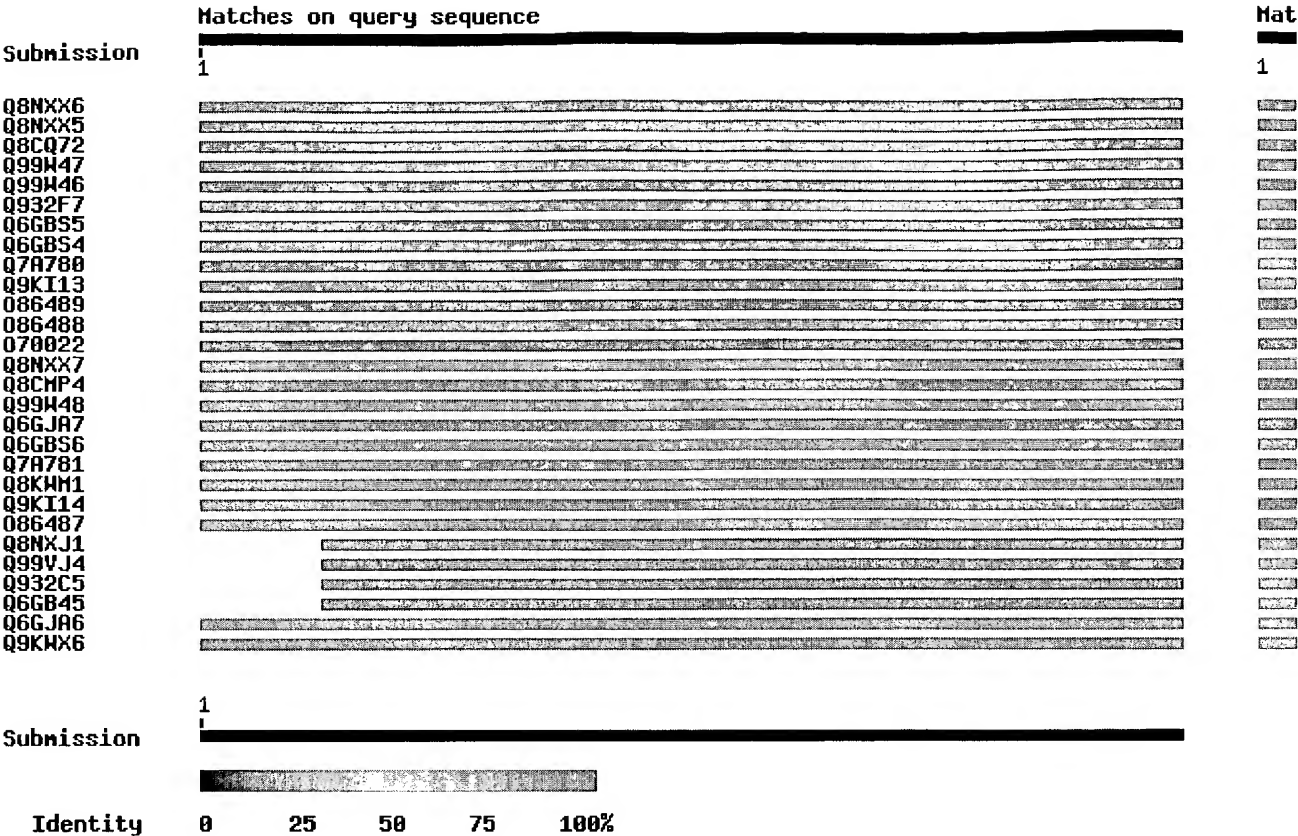
<input type="checkbox"/>	tr <a href="#">O86489</a>	Sdr E protein [sdr E] [Staphylococcus aureus]	<a href="#">34</a>	0.23
<input type="checkbox"/>	tr <a href="#">O86488</a>	SdrD protein [sdrD] [Staphylococcus aureus]	<a href="#">34</a>	0.23
<input type="checkbox"/>	tr <a href="#">O70022</a>	Fibrinogen-binding protein precursor [Staphylococcus e...	<a href="#">34</a>	0.23
<input type="checkbox"/>	tr <a href="#">Q8NXX7</a>	Ser-Asp rich fibrinogen-binding bone sialoprotein-bind...	<a href="#">32</a>	1.3
<input type="checkbox"/>	tr <a href="#">Q8CMP4</a>	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bind...	<a href="#">32</a>	1.3
<input type="checkbox"/>	tr <a href="#">Q99W48</a>	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	<a href="#">32</a>	1.3
<input type="checkbox"/>	tr <a href="#">Q6GJA7</a>	Putative surface anchored protein [sdrC] [Staphylococc...	<a href="#">32</a>	1.3
<input type="checkbox"/>	tr <a href="#">Q6GBS6</a>	Putative surface anchored protein [SAS0519] [Staphyloc...	<a href="#">32</a>	1.3
<input type="checkbox"/>	tr <a href="#">Q7A781</a>	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	<a href="#">32</a>	1.3
<input type="checkbox"/>	tr <a href="#">Q8KWM1</a>	Surface protein SdrI [Staphylococcus saprophyticus]	<a href="#">32</a>	1.3
<input type="checkbox"/>	tr <a href="#">Q9KI14</a>	Putative cell-surface adhesin SdrF [sdrF] [Staphylococ...	<a href="#">32</a>	1.3
<input type="checkbox"/>	tr <a href="#">O86487</a>	Sdrc protein [sdrc] [Staphylococcus aureus]	<a href="#">32</a>	1.3
<input type="checkbox"/>	tr <a href="#">Q8NXJ1</a>	Fibrinogen-binding protein [clfA] [Staphylococcus aure...	<a href="#">31</a>	1.8
<input type="checkbox"/>	tr <a href="#">Q99VJ4</a>	Fibrinogen-binding protein A, clumping factor [clfA] [...	<a href="#">31</a>	1.8
<input type="checkbox"/>	tr <a href="#">Q932C5</a>	Fibrinogen-binding protein [fnb] [Staphylococcus aureu...	<a href="#">31</a>	1.8
<input type="checkbox"/>	tr <a href="#">Q6GB45</a>	Clumping factor [SAS0752] [Staphylococcus aureus subsp...	<a href="#">31</a>	1.8
<input type="checkbox"/>	tr <a href="#">Q6GJA6</a>	Bone sialoprotein-binding protein [bbp] [Staphylococcu...	<a href="#">30</a>	4.4
<input type="checkbox"/>	tr <a href="#">Q9KWX6</a>	Bone sialoprotein-binding protein [bbp] [Staphylococcu...	<a href="#">30</a>	4.4

## Graphical overview of the alignments

[Click here](#)to resubmit your query after masking regions matching [PROSITE](#) profiles or Pfam HMMs([Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits

Pfam hits



Alignments

tr Q8NXX6 Ser-Asp rich fibrinogen-binding bone sialoprotein-binding protein [sdrD] [Staphylococcus aureus (strain MW2)] 1347 AA align

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 339 TYTFTDYVD 347

tr Q8NXX5 Ser-Asp rich fibrinogen-binding bone sialoprotein-binding protein [sdrE] [Staphylococcus aureus (strain MW2)] 1141 AA align

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 365 TYTFTDYVD 373

tr Q8CQ72 **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding** 1056  
**protein** AA  
**[SE0331] [Staphylococcus epidermidis ATCC 12228]** [align](#)

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 372 TYTFTDYVD 380

tr Q99W47 **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding** 1385  
**protein** AA  
**[sdrD] [Staphylococcus aureus (strain Mu50 / ATCC** [align](#)  
**700699)]**

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 339 TYTFTDYVD 347

tr Q99W46 **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding** 1141  
**protein** AA  
**[sdrE] [Staphylococcus aureus (strain N315)]** [align](#)

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 365 TYTFTDYVD 373

tr Q932F7 **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding** 1141  
**protein** AA  
**[sdrE] [Staphylococcus aureus (strain Mu50 / ATCC** [align](#)  
**700699)]**

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 365 TYTFTDYVD 373

tr Q6GBS5 **Putative surface anchored protein [SAS0520] [Staphylococcus** 1365



**aureus**  
**subsp. aureus MSSA476]**

AA  
[align](#)

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 339 TYTFTDYVD 347

tr [Q6GBS4](#) **Bone sialoprotein-binding protein [SAS0521] [Staphylococcus aureus subsp. aureus MSSA476]**

1141  
AA  
[align](#)

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 365 TYTFTDYVD 373

tr [Q7A780](#) **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein [sdrD] [Staphylococcus aureus (strain N315)]**

1385  
AA  
[align](#)

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 339 TYTFTDYVD 347

tr [Q9KI13](#) **Fibrinogen-binding protein SdrG [sdrG] [Staphylococcus epidermidis]**

931  
AA  
[align](#)

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 370 TYTFTDYVD 378

tr [O86489](#) **Sdr E protein [sdr E] [Staphylococcus aureus]** 1166 AA

[align](#)

Score = 34.1 bits (73), Expect = 0.23

Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 370 TYTFTDYVD 378

tr O86488 SdrD protein [sdrD] [Staphylococcus aureus] 1315 AA

align

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 339 TYTFTDYVD 347

tr O70022 Fibrinogen-binding protein precursor [Staphylococcus  
epidermidis]

1092  
AA  
align

Score = 34.1 bits (73), Expect = 0.23  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9  
TYTFTDYVD  
Sbjct: 372 TYTFTDYVD 380

tr Q8NXX7 Ser-Asp rich fibrinogen-binding bone sialoprotein-binding  
protein  
[sdrC] [Staphylococcus aureus (strain MW2)]

955  
AA  
align

Score = 31.6 bits (67), Expect = 1.3  
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9  
TYTFT+YVD  
Sbjct: 281 TYTFTNYVD 289

tr Q8CMP4 Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding  
protein  
[SE2395] [Staphylococcus epidermidis]

1633  
AA  
align

Score = 31.6 bits (67), Expect = 1.3  
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9

TYTFT+YVD  
Sbjct: 460 TYTFTNYVD 468

tr [Q99W48](#) **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein** 953  
[sdrC] [Staphylococcus aureus (strain Mu50 / ATCC 700699)] AA [align](#)

Score = 31.6 bits (67), Expect = 1.3  
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9  
TYTFT+YVD  
Sbjct: 281 TYTFTNYVD 289

tr [Q6GJA7](#) **Putative surface anchored protein [sdrC] [Staphylococcus aureus subsp. aureus MRSA252]** 906  
AA [align](#)

Score = 31.6 bits (67), Expect = 1.3  
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9  
TYTFT+YVD  
Sbjct: 272 TYTFTNYVD 280

tr [Q6GBS6](#) **Putative surface anchored protein [SAS0519] [Staphylococcus aureus subsp. aureus MSSA476]** 957  
AA [align](#)

Score = 31.6 bits (67), Expect = 1.3  
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9  
TYTFT+YVD  
Sbjct: 281 TYTFTNYVD 289

tr [Q7A781](#) **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein** 953  
[sdrC] [Staphylococcus aureus (strain N315)] AA [align](#)

Score = 31.6 bits (67), Expect = 1.3  
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9  
TYTFT+YVD  
Sbjct: 281 TYTFTNYVD 289

tr Q8KWM1 Surface protein SdrI [Staphylococcus saprophyticus] 1893 AA

align

Score = 31.6 bits (67), Expect = 1.3  
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9  
TYTFT+YVD  
Sbjct: 537 TYTFTNYVD 545

tr Q9KI14 Putative cell-surface adhesin SdrF [sdrF] [Staphylococcus epidermidis] 1733 AA

align

Score = 31.6 bits (67), Expect = 1.3  
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9  
TYTFT+YVD  
Sbjct: 460 TYTFTNYVD 468

tr Q86487 SdrC protein [sdrC] [Staphylococcus aureus] 947 AA

align

Score = 31.6 bits (67), Expect = 1.3  
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9  
TYTFT+YVD  
Sbjct: 281 TYTFTNYVD 289

tr Q8NXJ1 Fibrinogen-binding protein [clfA] [Staphylococcus aureus (strain MW2)] 946 AA

align

Score = 31.2 bits (66), Expect = 1.8  
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 YTFPTYVD 9  
YTFPTYVD  
Sbjct: 316 YTFPTYVD 323

tr Q99VJ4 **Fibrinogen-binding protein A, clumping factor [clfA]** 989 AA  
[**Staphylococcus aureus (strain N315)**]

align

Score = 31.2 bits (66), Expect = 1.8  
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 YTFTDYVD 9  
YTFTDYVD  
Sbjct: 317 YTFTDYVD 324

tr Q932C5 **Fibrinogen-binding protein [fnb]** [Staphylococcus aureus  
(strain **Mu50** / ATCC 700699)]

935  
AA  
align

Score = 31.2 bits (66), Expect = 1.8  
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 YTFTDYVD 9  
YTFTDYVD  
Sbjct: 317 YTFTDYVD 324

tr Q6GB45 **Clumping factor [SAS0752]** [Staphylococcus aureus subsp. aureus  
**MSSA476**]

align

Score = 31.2 bits (66), Expect = 1.8  
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 YTFTDYVD 9  
YTFTDYVD  
Sbjct: 316 YTFTDYVD 323

tr Q6GJA6 **Bone sialoprotein-binding protein [bbp]** [Staphylococcus  
aureus  
subsp. aureus MRSA252]

1137  
AA  
align

Score = 29.9 bits (63), Expect = 4.4  
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 1 TYTFTDYVD 9  
TY FTDYVD  
Sbjct: 365 TYKFTDYVD 373

tr Q9KWX6 **Bone sialoprotein-binding protein [bbp]** [Staphylococcus  
aureus]

1171  
AA  
align

Score = 29.9 bits (63), Expect = 4.4  
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 1 TYTFTDYVD 9  
TY FTDYVD  
Sbjct: 365 TYKFTDYVD 373

Database: EXPASY/UniProt

Posted date: Jul 29, 2004 5:14 AM  
Number of letters in database: 486,583,783  
Number of sequences in database: 1,529,856

Lambda	K	H
0.333	0.284	1.87

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1  
Number of HSP's successfully gapped in prelim test: 0  
length of query: 9  
length of database: 486,583,783  
effective HSP length: 0  
effective length of query: 9  
effective length of database: 486,583,783  
effective search space: 4379254047  
effective search space used: 4379254047  
T: 16  
A: 40  
X1: 15 ( 7.2 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 41 (21.5 bits)  
S2: 61 (29.1 bits)

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Mark Patent

Mark Range

Mark Section

7

of 83

All Sections

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## First Hit

ODP!

L6: Entry 7 of 83

File: PGPB

Feb 26, 2004

PGPUB-DOCUMENT-NUMBER: 20040038327  
PGPUB-FILING-TYPE: new  
DOCUMENT-IDENTIFIER: US 20040038327 A1

TITLE: Antibodies to polypeptides from coagulase-negative staphylococci

PUBLICATION-DATE: February 26, 2004

## INVENTOR - INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Foster, Timothy J.	Dublin	TX	IE	
McCrea, Kirk	Houston	TX	US	
Hook, Magnus A.O.	Houston	TX	US	
Davis, Stacey	Houston		US	
Ni Eidhin, Deirdre	Dublin		IE	
Hartford, Orla	Meath		IE	

US-CL-CURRENT: 435/7.32; 530/388.4

### CLAIMS :

What is claimed is:

1. An isolated antibody that binds to the SdrG fibrinogen-binding protein from coagulase-negative Staphylococcus epidermidis.
2. The isolated antibody according to claim 1 wherein the protein is cell-wall associated, and binds both soluble and immobilized fibrinogen.
3. The isolated antibody according to claim 1 wherein the antibody recognizes a protein that is cell wall-associated, exhibits cation-dependent ligand-binding and has a highly conserved motif of which the consensus sequence is TYTFTDYVD (SEQ ID NO: 16).
4. The isolated antibody according to claim 1 which is raised against the SdrG fibrinogen-binding protein from coagulase-negative Staphylococcus epidermidis.
5. The isolated antibody according to claim 1 which is raised against the A region of the SdrG fibrinogen-binding protein from coagulase-negative Staphylococcus epidermidis.
6. The isolated antibody according to claim 1 wherein the SdrG fibrinogen-binding protein comprises SEQ ID NO:10.
7. The isolated antibody according to claim 1 wherein the SdrG fibrinogen-binding protein is encoded by the nucleic acid comprising SEQ ID NO:7.



- 8. An isolated antibody that is reactive with the ligand binding A region of the SdrG fibrinogen-binding protein from coagulase-negative Staphylococcus epidermidis.
- 9. A diagnostic kit comprising the antibody according to claim 1 and a means for identifying binding by said antibody.
- 10. Isolated antisera containing the antibody according to claim 1.
- 11. A diagnostic kit comprising antibodies reactive with an SdrG protein from coagulase-negative Staphylococcus epidermidis which is cell-wall associated and which binds both soluble and immobilized fibrinogen.
- 12. A diagnostic kit comprising an antibody reactive with a protein that is cell wall-associated, exhibits cation-dependent ligand-binding and has a highly conserved motif of which the consensus sequence is TYTFTDYVD (SEQ ID NO: 16), wherein the protein is isolated from coagulase-negative Staphylococcus epidermidis.
- 13. An isolated antibody reactive with a protein that is cell wall-associated, exhibits cation-dependent ligand-binding and has a highly conserved motif of which the consensus sequence is TYTFTDYVD (SEQ ID NO: 16), wherein the protein is isolated from coagulase-negative Staphylococcus epidermidis.
- 14. An isolated antibody according to claim 13 wherein the protein comprises the SdrG fibrinogen-binding protein isolated from coagulase-negative Staphylococcus epidermidis.
- 15. An isolated antibody according to claim 13 wherein the protein comprises the ligand binding A region of the SdrG fibrinogen-binding protein isolated from coagulase-negative Staphylococcus epidermidis.

## First Hit

Feb 26, 2004

PGPUB-DOCUMENT-NUMBER: 20040038327  
PGPUB-FILING-TYPE: new  
DOCUMENT-IDENTIFIER: US 20040038327 A1

TITLE: Antibodies to polypeptides from coagulase-negative staphylococci

PUBLICATION-DATE: February 26, 2004

## INVENTOR - INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Foster, Timothy J.	Dublin	TX	IE	
McCrea, Kirk	Houston	TX	US	
Hook, Magnus A.O.	Houston	TX	US	
Davis, Stacey	Houston		US	
Ni Eidhin, Deirdre	Dublin		IE	
Hartford, Orla	Meath		IE	

APPL-NO: 10/ 615383 [PALM]  
DATE FILED: July 9, 2003

RELATED-US-APPL-DATA:

Application 10/615383 is a division-of US application 09/386962, filed August 31, 1999, US Patent No. 6635473

INT-CL: [07] G01 N 33/554, G01 N 33/569, C07 K 16/12

US-CL-PUBLISHED: 435/7.32; 530/388.4  
US-CL-CURRENT: 435/7.32; 530/388.4

REPRESENTATIVE-FIGURES: NONE

ABSTRACT:

Antibodies reactive with isolated proteins, designated SdrF, SdrG and SdrH, and their corresponding amino acid and nucleic acid sequences, are provided which are useful in the prevention and treatment of infection caused by coagulase-negative staphylococcal bacteria such as S. epidermidis. The SdrF, SdrG and SdrH proteins are cell-wall associated proteins that specifically bind host proteins and which each have a highly conserved motif of which the consensus sequence is TYTFTDYVD (SEQ ID NO: 16). The antibodies are also useful for the diagnosis and treatment of coagulase-negative staphylococcal infections and may be administered to wounds or used to coat biomaterials to act as blocking agents to prevent or inhibit the binding of coagulase-negative staphylococci to wounds or biomaterials.

## CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a divisional application of U.S. Appln. Ser. No.

09/386,962, filed Aug. 31, 1999, and claims the benefit of U.S. Provisional Applications Serial No. 60/117,119, filed Jan. 25, 1999, and Serial No. 60/098,443, filed Aug. 31, 1998.

## Freeform Search

Updated  
8/4/2004  
VBP

Database:

US Pre-Grant Publication Full-Text Database  
 US Patents Full-Text Database  
 US OCR Full-Text Database  
 EPO Abstracts Database  
 JPO Abstracts Database  
 Derwent World Patents Index  
 IBM Technical Disclosure Bulletins

Term:

L2 near10 (antibodies or antisera or  
 monoclonal or polyclonal or antiserum or mono-  
 clonal or ig or immune or immunoglobulin)

Display:

50

Documents in Display Format: KWIC

Starting with Number

1

 Generate: ☐ Hit List ☒ Hit Count ☐ Side by Side ☐ Image

Search

Clear

Interrupt

## Search History

 DATE: Wednesday, August 04, 2004 [Printable Copy](#) [Create Case](#)

Set  
 Name Query  
 side by  
 side /

Hit  
 Count Set  
 Name  
 result set

DB=USPT; PLUR=YES; OP=AND

L1 mscramm.clm.

0 L1

L2 mscramm

22 L2

 L3 L2 near10 (antibodies or antisera or monoclonal or polyclonal or antiserum  
 or mono-clonal or ig or immune or immunoglobulin)

4 L3

END OF SEARCH HISTORY

## WEST Search History

DATE: Wednesday, August 04, 2004

Hide?	Set Name	Query	Hit Count
		<i>DB=USPT; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L1	clump\$ near3 factor\$	69
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L2	clump\$-near3-factor\$	122
<input type="checkbox"/>	L3	clf or clfa or clf-a	5903
<input type="checkbox"/>	L4	(L3 or l2 or l1) and (staph or staphyloc\$ or aureus! or epidermidis)	122
<input type="checkbox"/>	L5	L4 and (man or woman or homosap\$ or human\$)	96
<input type="checkbox"/>	L6	L5 and (antibod\$ or antiser\$ or anti-ser\$ or ivig or iv-ig or iggiv or igg-iv or immunoglob\$ or globulin)	83
		<i>DB=PGPB; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L7	US-20030099656-A1.did.	1
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L8	(l1 or l6) and (patti or foster or hook).in.	22

END OF SEARCH HISTORY

*Inventor search*

[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 22 of 22 returned.**

- 
- ☐ 1. [20040142348](#). 21 Oct 03. 22 Jul 04. Proteins and polypeptides from coagulase-negative staphylococci. Foster, Timothy J., et al. 435/6; 435/252.3 435/320.1 435/69.1 530/350 536/23.7 C12Q001/68 C07H021/04 C07K014/31.
- 
- ☐ 2. [20040141997](#). 21 Oct 03. 22 Jul 04. Methods for treating or preventing infections from coagulase-negative staphylococci. Foster, Timothy J., et al. 424/190.1; 514/44 A61K048/00 A61K039/02.
- 
- ☐ 3. [20040101919](#). 15 Sep 03. 27 May 04. Bioinformatic method for identifying surface-anchored proteins from gram-positive bacteria and proteins obtained thereby. Hook, Magnus, et al. 435/7.32; G01N033/554 G01N033/569.
- 
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NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402 (1997).

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<input type="checkbox"/>	tr Q53599	MHC class II analog [Staphylococcus aureus]	1229	0.0
<input type="checkbox"/>	tr Q9S2Z4	Cell surface protein map-w precursor [map-w] [Staphylo...	979	0.0
<input type="checkbox"/>	tr O07318	Outer surface binding 70kD protein (Fragment) [Staphyl...	918	0.0
<input type="checkbox"/>	tr Q9K4S8	Map-ND2C protein precursor [map-ND2C] [Staphylococcus ...	910	0.0
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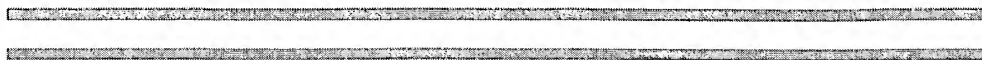
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<input type="checkbox"/>	tr	Q7A090	MW2130 protein [MW2130] [Staphylococcus aureus (strain...	83	1e-14
<input type="checkbox"/>	tr	Q8G961	Hypothetical protein ORF9 [ORF9] [Staphylococcus aureus]	83	1e-14
<input type="checkbox"/>	tr	Q7RJV0	CCAAT-box DNA binding protein subunit B, putative (Fra...	54	7e-06
<input type="checkbox"/>	tr	Q6LFF0	Hypothetical protein [MAL6P1.307] [Plasmodium falcipar...	54	9e-06
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<input type="checkbox"/>	tr	Q7RS53	Hypothetical protein [PY00512] [Plasmodium yoelii yoelii]	47	0.001
<input type="checkbox"/>	tr	Q7RK24	Hypothetical protein [PY03080] [Plasmodium yoelii yoelii]	47	0.001
<input type="checkbox"/>	tr	Q99WH4	Exotoxin 13 [set13] [Staphylococcus aureus (strain Mu5...	47	0.002
<input type="checkbox"/>	tr	Q7A7H2	Exotoxin 13 [set13] [Staphylococcus aureus (strain N315)]	47	0.002
<input type="checkbox"/>	tr	Q8ILS9	Hypothetical protein [PF14_0165] [Plasmodium falciparu...	47	0.002
<input type="checkbox"/>	tr	Q7RR45	Hypothetical protein [PY00892] [Plasmodium yoelii yoelii]	47	0.002
<input type="checkbox"/>	tr	Q97TE6	Hypothetical protein CAP0158 [CAP0158] [Clostridium ac...	46	0.003
<input type="checkbox"/>	tr	Q9RN33	Exotoxin 1 [set1] [Staphylococcus aureus]	46	0.003
<input type="checkbox"/>	tr	Q9RN32	Exotoxin 1 [set1] [Staphylococcus aureus]	45	0.003
<input type="checkbox"/>	tr	Q8IL30	Hypothetical protein [PF14_0419] [Plasmodium falciparu...	45	0.003
<input type="checkbox"/>	tr	Q7RNU0	Hypothetical protein [PY01725] [Plasmodium yoelii yoelii]	45	0.003
<input type="checkbox"/>	tr	Q8IL12	Hypothetical protein [PF14_0438] [Plasmodium falciparu...	45	0.004
<input type="checkbox"/>	tr	Q8NY46	Set24 protein [set24] [Staphylococcus aureus (strain M...	45	0.006
<input type="checkbox"/>	tr	Q6GC56	Exotoxin 5 [SAS0392] [Staphylococcus aureus subsp. aur...	45	0.006
<input type="checkbox"/>	tr	Q8IJA2	Hypothetical protein [PF10_0296] [Plasmodium falciparu...	45	0.006
<input type="checkbox"/>	tr	Q7RR36	Methlytransferase, UbiE/COQ5 family [PY00901] [Plasmod...	45	0.006
<input type="checkbox"/>	tr	Q8I3J8	Hypothetical protein [PFE1330c] [Plasmodium falciparum...	44	0.007

<input type="checkbox"/>	tr	<a href="#">Q8I2A4</a>	Hypothetical protein PFA0180w [PFA0180w] [Plasmodium f...	<a href="#">44</a>	0.007
<input type="checkbox"/>	tr	<a href="#">Q7RM00</a>	Similar to sentrin/SUMO-specific protease [PY02388] [P...	<a href="#">44</a>	0.007
<input type="checkbox"/>	tr	<a href="#">Q8JKP9</a>	Stress-induced protein STI1 [orf62] [Heliothis zea vir...	<a href="#">44</a>	0.010
<input type="checkbox"/>	tr	<a href="#">Q8NY48</a>	Set22 protein [set22] [Staphylococcus aureus (strain M...	<a href="#">44</a>	0.010
<input type="checkbox"/>	tr	<a href="#">Q9ZHL0</a>	Large supernatant protein 2 [lspA2] [Haemophilus ducreyi]	<a href="#">44</a>	0.010
<input type="checkbox"/>	tr	<a href="#">Q6GC58</a>	Exotoxin 1 [SAS0390] [Staphylococcus aureus subsp. aur...	<a href="#">44</a>	0.010
<input type="checkbox"/>	tr	<a href="#">Q7BY44</a>	Large supernatant protein 2 [lspA2] [Haemophilus ducre...	<a href="#">44</a>	0.010
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<input type="checkbox"/>	tr	<a href="#">Q8IHV8</a>	Hypothetical protein [PF11_0418] [Plasmodium falciparu...	<a href="#">44</a>	0.010
<input type="checkbox"/>	tr	<a href="#">Q7REY3</a>	235 kDa rhoptry protein (Fragment) [PY04930] [Plasmodi...	<a href="#">44</a>	0.010
<input type="checkbox"/>	tr	<a href="#">Q97277</a>	Kinesin, putative [MAL3P7.1] [Plasmodium falciparum (i...	<a href="#">44</a>	0.010
<input type="checkbox"/>	tr	<a href="#">Q9PQ08</a>	Hypothetical protein UU482 [UU482] [Ureaplasma parvum ...	<a href="#">44</a>	0.013
<input type="checkbox"/>	tr	<a href="#">Q7RKX6</a>	Synthetic antigen of P.falciparum, putative (Fragment)...	<a href="#">44</a>	0.013
<input type="checkbox"/>	tr	<a href="#">Q7RDD8</a>	Hypothetical protein [PY05484] [Plasmodium yoelii yoelii]	<a href="#">44</a>	0.013
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<input type="checkbox"/>	tr	<a href="#">Q9ZFS5</a>	Exotoxin 1 [set1] [Staphylococcus aureus]	<a href="#">43</a>	0.017
<input type="checkbox"/>	tr	<a href="#">Q8ID19</a>	Hypothetical protein PF13_0360 [PF13_0360] [Plasmodium...	<a href="#">43</a>	0.017
<input type="checkbox"/>	tr	<a href="#">Q7RH89</a>	Asparagine-rich protein [PY04100] [Plasmodium yoelii y...	<a href="#">43</a>	0.017
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<input type="checkbox"/>	tr	<a href="#">Q8IC44</a>	Starp antigen [PF07_0006] [Plasmodium falciparum (isol...	<a href="#">43</a>	0.022
<input type="checkbox"/>	tr	<a href="#">Q8I5Q0</a>	Hypothetical protein [PFL0755c] [Plasmodium falciparum...	<a href="#">43</a>	0.022
<input type="checkbox"/>	tr	<a href="#">Q7R9P1</a>	Hypothetical protein (Fragment) [PY06820] [Plasmodium ...	<a href="#">43</a>	0.022
<input type="checkbox"/>	sp	<a href="#">P38537</a>	SLAP_BACSH Surface-layer 125 kDa protein precursor [Ba...	<a href="#">42</a>	0.028
<input type="checkbox"/>	sp	<a href="#">P55746</a>	CGA2_HELPY Cytotoxicity associated immunodominant anti...	<a href="#">42</a>	0.028
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<input type="checkbox"/>	tr	<a href="#">Q9BJY0</a>	235 kDa rhoptry protein (Fragment) [IIIa.1] [Plasmodiu...	<a href="#">42</a>	0.028
<input type="checkbox"/>	tr	<a href="#">Q898L8</a>	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4....	<a href="#">42</a>	0.037
<input type="checkbox"/>	tr	<a href="#">Q7XVF0</a>	OSJNBa0083D01.8 protein [OSJNBa0083D01.8] [Oryza sativ...	<a href="#">42</a>	0.037
<input type="checkbox"/>	tr	<a href="#">Q8IKG8</a>	Rhoptry protein, putative [PF14_0637] [Plasmodium falc...	<a href="#">42</a>	0.037
<input type="checkbox"/>	tr	<a href="#">Q8IHP9</a>	Hypothetical protein [PF11_0480] [Plasmodium falciparu...	<a href="#">42</a>	0.037
<input type="checkbox"/>	tr	<a href="#">Q8I469</a>	Hypothetical protein [PFE0155w] [Plasmodium falciparum...	<a href="#">42</a>	0.037
<input type="checkbox"/>	tr	<a href="#">Q7YXS0</a>	MB2 (Fragment) [Plasmodium gallinaceum]	<a href="#">42</a>	0.037
<input type="checkbox"/>	tr	<a href="#">Q7RRK2</a>	Protein kinase domain, putative [PY00717] [Plasmodium ...	<a href="#">42</a>	0.037
<input type="checkbox"/>	tr	<a href="#">Q7RND4</a>	Chloroquine resistance marker protein (Fragment) [PY01...	<a href="#">42</a>	0.037
<input type="checkbox"/>	sp	<a href="#">Q7TUA3</a>	FMT_PROMP Methionyl-tRNA formyltransferase (EC 2.1.2.9...	<a href="#">42</a>	0.048
<input type="checkbox"/>	tr	<a href="#">Q841F4</a>	Iron-regulated outer membrane protein (Fragment) [fetA...	<a href="#">42</a>	0.048
<input type="checkbox"/>	tr	<a href="#">Q8IL70</a>	Hypothetical protein [PF14_0379] [Plasmodium falciparu...	<a href="#">42</a>	0.048
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<input type="checkbox"/>	tr	<a href="#">Q8I437</a>	Hypothetical protein [PFE0320w] [Plasmodium falciparum...	<a href="#">42</a>	0.048
<input type="checkbox"/>	tr	<a href="#">Q7RJT3</a>	Kinesin-like protein K6 [PY03174] [Plasmodium yoelii y...	<a href="#">42</a>	0.048
<input type="checkbox"/>	tr	<a href="#">Q6H1A0</a>	Adhesin (Fragment) [hmw2A] [Haemophilus influenzae]	<a href="#">41</a>	0.063
<input type="checkbox"/>	tr	<a href="#">Q841B7</a>	Iron-regulated outer membrane protein (Fragment) [fetA...	<a href="#">41</a>	0.063
<input type="checkbox"/>	tr	<a href="#">Q8IIV3</a>	Hypothetical protein [PF11_0060] [Plasmodium falciparu...	<a href="#">41</a>	0.063
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<input type="checkbox"/>	tr	<a href="#">Q8IEH7</a>	Hypothetical protein PF13_0079 [PF13_0079] [Plasmodium...	<a href="#">41</a>	0.063

**Graphical overview of the alignments**[Click here](#)

to resubmit your query after masking regions matching PROSITE profiles  
or Pfam HMMs

([?](#) Help) (use ScanProsite for more details about PROSITE matches)

**Profile hits****Pfam hits**



Submission	Matches on query sequence					Mat
	1				500	
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Q53599						
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CGA2_HELPY						
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## Alignments

tr Q6GFB8 MHC class II analog [SAR2030] [Staphylococcus aureus subsp. aureus  
MRSA252] 689  
AA  
align

Score = 1290 bits (3337), Expect = 0.0  
Identities = 668/689 (96%), Positives = 668/689 (96%)

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Sbjct: 1 MKFKSLITTTALGVLASTGANFNTNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT 60

Query: 61 SQNILSSLTFNKNQQISYKDIENTKVKSVLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV 120  
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Sbjct: 61 SQNILSSLTFNKNQQISYKDIENTKVKSVLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV 120

Query: 121 DLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVPYTITVNGTSQNILSNLTF 180  
DLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVPYTITVNGTSQNILSNLTF  
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tr Q9Z4P5 MapN protein precursor [mapN] [Staphylococcus aureus] 689 AA  
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Score = 1287 bits (3331), Expect = 0.0  
Identities = 666/689 (96%), Positives = 668/689 (96%)

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Query: 61 SQNILSSLTFNKNQQISYKDIENTKVSPLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV 120  
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Query: 661 KFVDLKAQKQDSKVFKATDIKKVDIEIKF 689  
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tr Q53599 MHC class II analog [Staphylococcus aureus] 689 AA  
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Score = 1229 bits (3179), Expect = 0.0

Identities = 635/689 (92%), Positives = 648/689 (93%)

```

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Query: 241 LINTGDIKNININVETKKQAKDKEAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN 300
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Query: 301 LTAKVKSVLKSDRGVSRDLKHAKKAYYTVYFKNGGKRVIHLSNIIYTANLVHAKDIKKI 360
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Query: 361 EVTVKTGSKANAERYVPYTI AVNGTSTPNLSDLKFKGDSRVSYSIDITKKVKSVLKYDRGI 420
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Query: 421 GERELKYAKKATYTVHFKNGTKKVINLNSKISQLNLLFXXXXXXXXXXXXTGSKAKADSY 480
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Sbjct: 421 GERELKYAEKATYTVHFKNGTKKVINLNSNISQLNLLYVKDIKNIDIDVKTGAKAKVYSY 480

Query: 481 VPYTI AVNGTSTPIASKLKL SNKQLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYTV 540
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Query: 541 HFKNGKTQVVDLKS DIFTRNLFSVXXXXXXXXXXVKQHTKSNKALNKVSNIATKVKFPVTI 600
          HFKNGKTQVVDLKS DIFTRNLFSV VKQ +KSNKALNKV+N ATKVKFPVTI
Sbjct: 541 HFKNGKTQVVDLKS DIFTRNLFSVKDIKKIDINVKQQSKSNKALNKVTNKATKVKFPVTI 600

Query: 601 NGFSNVVSNEFAFLHPHKITTNDLNAKLRLALASDQGITKHDIGLSERTVYKVYFKDGSS 660
          NGFSN+VSNEFAFLHPHKITTNDLNAKLRLAL SDQGITKHDIGLSERTVYKVYFKDGSS
Sbjct: 601 NGFSNLVSNEFAFLHPHKITTNDLNAKLRLALASDQGITKHDIGLSERTVYKVYFKDGSS 660

Query: 661 KFVDLKAQKQDSKVFKATDIKKVDIEIKF 689
          K DLKAQKQDSKVFKATDIKKVDIEIKF
Sbjct: 661 KLEDLKAQKQDSKVFKATDIKKVDIEIKF 689

```

tr Q9S2Z4 Cell surface protein map-w precursor [map-w] [Staphylococcus 687 AA

aureus]

align

Score = 979 bits (2530), Expect = 0.0

Identities = 510/688 (74%), Positives = 580/688 (84%), Gaps = 10/688 (1%)

Query: 1 MKFKSLITTTLALGVLASTGANFNTNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT 60  
 MKFKSLITTTLALGV+ASTGANFNTNEASAAAK +DKSSS+LHHG+S IQIPYTITVNGT  
 Sbjct: 1 MKFKSLITTTLALGVIASTGANFNTNEASAAAKPLDKSSSTLHHGHSNIQIPYTITVNGT 60

Query: 61 SQNILSSLTFNKNQQISYKDIENTKVKSVLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV 120  
 SQNILSSLTFNKNQ ISYKDIENTKVKSVLYFNRGISDIDLRLSKQA+YTVHFKNGTKRV+  
 Sbjct: 61 SQNILSSLTFNKNQNISYKDIENTKVKSVLYFNRGISDIDLRLSKQAEYTVHFKNGTKRVI 120

Query: 121 DLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVPYTITVNGTSQNILSNLTF 180  
 DLK+GI+TADLINTSDIKAISVNVDTKKQ KDK AKANVQVPYTITVNGTSQNILSNLTF  
 Sbjct: 121 DLKSGIYTADLINTSDIKAISVNVDTKKQPKDK-AKANVQVPYTITVNGTSQNILSNLTF 179

Query: 181 KKNQQISYKDLENNVKS SVLKS NRGITD VDLRLSKQAKFTVNFKNGT KKVIDLKAGIYTAN 240  
 KNQ ISYKDLE+ VKSVL+SNRGITD VDLRLSKQAK+TVNFKNGT KKVIDLKAGIYTAN  
 Sbjct: 180 NKNQNISYKDLEDKVKSVLESNRGITD VDLRLSKQAKYTVNFKNGT KKVIDLKAGIYTAN 239

Query: 241 LINTGDIKNININVETKKQAKDKAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN 300  
 LIN+ DIK+ININV+TKK ++K AK N QVPYSINLNGT+TNI SNL+FSNKPWTNYKN  
 Sbjct: 240 LINSSDIKSININVDTKKHIENK-AKRNYQVPYSINLNGTSTNILSNLSFSNKPWTNYKN 298

Query: 301 LTAKVKS SVLKSDRGVSE RDLKHAKAYYTVYFKNGGK RVIHLNSNIYTANLVHAKDIKKI 360  
 LT+++KSVLK DRG+SE+DLK+AKKAYYTVYFKNGGK R++ LNS YTANLVH KD+K+I  
 Sbjct: 299 LTSQIKSVLKHDRGISEQDLKYAKKAYYTVYFKNGGKRILQLNSKNYTANLVHV KDV KRI 358

Query: 361 EVTVKTGSKANAERYVPYTI AVNGTSTPNLS DLKFKGDSRVSYSDITKKVKS SVLK YDRGI 420  
 E+TVKTG+KA A+RYVPYTI AVNGTSTP LSDLK FGD RV Y DITKKVKS SVLK+DRGI  
 Sbjct: 359 EITVKTGTAKADRYVPYTI AVNGTSTPILSDLKFTGDP RVGYKDITKKVKS SVLKHDRGI 418

Query: 421 GERELKYAKKATYTVHFKNGTKKVINLNSKISQLNLLFXXXXXXXXXXXXTGSKAKADSY 480  
 GERELKYAKKATYTVHFKNG KKVINLNSKISQLNLL+ TGSKAKADSY  
 Sbjct: 419 GERELKYAKKATYTVHFKNGKKKVINLNSKISQLNLLYVQDIKKIDIDVKTGSKAKADSY 478

Query: 481 VPYTI AVNGTSTPIASKLKL SNKQLIGYQDLNKKVKS SVLKHDRGINDIELKFAKQAKYTV 540  
 VPYTI AVNGTSTPI SKLK+SNKQLI Y+ LN KVKSVLK++RGI+D++LKF AKQAKYTV  
 Sbjct: 479 VPYTI AVNGTSTPILSKLKISNKQLISYKYLNDKVKSVLKNRGISDLDLKFAKQAKYTV 538

Query: 541 HFKNGKTQVVDLKS DIFTRNLFSVXXXXXXXXXXVKQHTKSNKALNKVSNIATKV KFPVTI 600  
 +FKNGK QVV+LKSDIFT NLFS VK +K + + V + + +  
 Sbjct: 539 YFKNGKKQVNLKSDIFT PNLFSAKDIKKIDIDVKTGSK-----AKADSYVPYTI AV 590

Query: 601 NGFSNVVSNEFAFLHPHKIT TNDLNAKLRLALASDQGITKH DIGLSERTVYKVYFKDGSS 660  
 NG S + ++ + I+ LN K++ L S++GI+ D+ +++ Y VYFK+G  
 Sbjct: 591 NGTSTPILSKLKISNKQLISYKYLNDKVKSVLKSERGISDLDLKFAKQAKYTVYFKNGKK 650

Query: 661 KFVDLKA AKQDSKVFKATDIKKVDIEIK 688  
 + V+LK+ +F A DIKK+DI++K  
 Sbjct: 651 QVNLKSDIFT PNLFSAKDIKKIDIDVK 678

Score = 652 bits (1681), Expect = 0.0

Identities = 340/559 (60%), Positives = 426/559 (75%), Gaps = 6/559 (1%)

Query: 24 NTNEASAAKQIDKSSSSSLHHGYSKIQIPYTITVNGTSQNILSSSLTFNKNQQISYKDIE 83  
NT++ A + +D + +Q+PYTITVNGTSQNILS+LTFNKNQ ISYKD+E+  
Sbjct: 133 NTSDIKAISVNVDTKKQPKDKAKANVQVPYTITVNGTSQNILSNLTFNKNQNISYKDLED 192

Query: 84 KVKSVLYFNRGISDIDLRLSKQAKYTVHFKNGTGRVVDLKGAIHTADLINTSDIKAISVN 143  
KVKSVL NRGID+DLRLSKQAKYTV+FKNGTK+V+DLKAGI+TA+LIN+SDIK+I++N  
Sbjct: 193 KVKSVLESNRGITDIDLRLSKQAKYTVNFKNGTKKVIDLKGAIYTANLINSSDIKSININ 252

Query: 144 VDTKKQVKDKAKANVQVPYTITVNGTSQNILSNLTFKKNQQISYKDLENNVKSVLKSNR 203  
VDTKK +++K AK N QVPY+I +NGTS NILSNL+F +YK+L + +KSVLK +R  
Sbjct: 253 VDTKKHIENK-AKRNYQVPYSINLNGTSTNILSNLSFSNKPWTNYKNLTSQIKSVLKHDR 311

Query: 204 GITDIDLRLSKQAKFTVNFKNGTKKVIDLKGAIYTANLINTGDIKNININVETKKQAKDK 263  
GI++ DL+ +K+A +TV FKNG K+++ L + YTANL++ D+K I I V+T  
Sbjct: 312 GISEQDLKYAKKAYYTVYFKNGGKRILQLNSKNYTANLVHVKDVKRIEITVKT-----GT 366

Query: 264 EAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKNLTAKVKSVLKSDRGVSEDLKHA 323  
+AKA+ VPY+I +NGT+T I S+L F+ P YK++T KVKSVLK DRG+ ER+LK+A  
Sbjct: 367 KAKADRYVPYTIANGTSTPILSDLKFTGDPVGVYKDITKKVKSVLKHDRGIGERELKYA 426

Query: 324 KKAYYTVYFKNGGKRVIHLSNIYTANLVHAKDIKKIEVTVKTGSKANAERYVPYTIAVN 383  
KKA YTV+FKNG K+VI+LNS I NL++ +DIKKI++ VKTGSKA A+ YVPYTIAVN  
Sbjct: 427 KKATYTVHFKNKKVINLSKISQLNLLYVQDIKKIDIDVKTGSKAKADSYVPYTIAVN 486

Query: 384 GTSTPNLSDLKFKGDSRVSYSIDITKKVKSVLKYDRGIGERELKYAKKATYTVHFKNGT 443  
GTSTP LS LK +SY + KVKSVLK +RGI + +LK+AK+A YTV+FKNG K+  
Sbjct: 487 GTSTPILSKLISNKQLISYKYLNDKVKSVLKNERGISDLDLKFAKQAKYTVYFKNGKKQ 546

Query: 444 VINLSKISQLNLLFXXXXXXXXXXXXTGSKAKADSYVPYTIAVNGTSTPIASKLKLSNK 503  
V+NL S I NL TGSKAKADSYVPYTIAVNGTSTPI SKLK+SNK  
Sbjct: 547 VVNLKSDIFTPNLFSADIKKIDIDVKTGSKAKADSYVPYTIAVNGTSTPILSKLKISNK 606

Query: 504 QLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYTVHFKNGTQVVDLKS DIFTRNLFS 563  
QLI Y+ LN KVKSVLK +RGI+D++LKFAKQAKYTV+FKNGK QVV+LKSDIFT NLFS  
Sbjct: 607 QLISYKYLNDKVKSVLKSERGISDLDLKFAKQAKYTVYFKNGKKQVVNLKSDIFTPNLFS 666

Query: 564 VXXXXXXXXXVKQHTKSNK 582  
VKQ+TKS K  
Sbjct: 667 AKDIKKIDIDVKQYTKSKK 685


Score = 318 bits (814), Expect = 3e-85  
Identities = 175/323 (54%), Positives = 229/323 (70%), Gaps = 12/323 (3%)

Query: 51 IPYTITVNGTSQNILSSSLTFNKNQQISYKDIEKVKSVLYFNRGISDIDLRLSKQAKYTV 110  
+PYTI VNGTS ILS L F + ++ YKDI KVKSVL +RGI + +L+ +K+A YTV  
Sbjct: 374 VPYTIANGTSTPILSDLKFTGDPVGVYKDITKKVKSVLKHDRGIGERELKYAKKATYTV 433

Query: 111 HFKNGTKRVVDLKGAIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVPYTITVNGT 170  
HFKNG K+V++L + I +L+ DIK I ++V T +AKA+ VPYTI VNGT  
Sbjct: 434 HFKNGKKVINLSKISQLNLLYVQDIKKIDIDVKT-----GSKAKADSYVPYTIANGT 488

Query: 171 SQNILSNLTFKKNQQISYKDLENNVKSVLKSNRGITDIDLRLSKQAKFTVNFKNGTKKVI 230  
S ILS L Q ISYK L + VKSVLK+ RGI+D+DL+ +KQAK+TV FKNG K+V+  
Sbjct: 489 STPILSKLKISNKQLISYKYLNDKVKSVLKNERGISDLDLKFAKQAKYTVYFKNGKKQVV 548

Query: 231 DLKAGIYTANLINTGDIKNININVETKKQAKDKAKANNQVPYSINLNGTTTNIQSNLAF 290  
+LK+ I+T NL + DIK I+I+V+T +AKA++ VPY+I +NGT+T I S L

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# NiceProt View of TrEMBL: Q9Z4P5

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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

*Note: most headings are clickable, even if they don't appear as links. They link to the [user manual](#) or [other documents](#).*

## Entry information

Entry name	<b>Q9Z4P5</b>
Primary accession number	<b>Q9Z4P5</b>
Secondary accession numbers	None
Entered in TrEMBL in	Release 10, May 1999
Sequence was last modified in	Release 10, May 1999
Annotations were last modified in	Release 26, March 2004
Name and origin of the protein	
Protein name	<b>MapN protein [Precursor]</b>
Synonyms	None
Gene name	<b>Name: mapN</b>
From	<i>Staphylococcus aureus</i> [TaxID: 1280]
Taxonomy	Bacteria; Firmicutes; Bacillales; <i>Staphylococcus</i> .

MHC II  
homolog

## References

- [1] SEQUENCE FROM NUCLEIC ACID.  
**STRAIN**=Newman;  
Hussain S.M., Herrmann M., Heilmann C., Peters G.;  
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

## Comments

None

## Cross-references

EMBL	AJ132841; CAA10802.1; -.[ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ]
InterPro	<a href="#">IPR005298</a> ; MAP. <a href="#">Graphical view of domain structure</a> .
Pfam	<a href="#">PF03642</a> ; MAP; 6. <a href="#">Pfam graphical view of domain structure</a> .
ProDom	<a href="#">[Domain structure / List of seq. sharing at least 1 domain]</a>
HOBACGEN	<a href="#">[Family / Alignment / Tree]</a>
ProtoMap	<a href="#">Q9Z4P5</a> .
PRESAGE	<a href="#">Q9Z4P5</a> .

ModBase

Q9Z4P5.

SMR

Q9Z4P5; CF88802B4F47C9CD.

SWISS-2DPAGE

Get region on 2D PAGE.


UniRef

View cluster of proteins with at least 50% / 90% identity.

Keywords

Signal.

Features



Feature table viewer

Key	From	To	Length	Description
SIGNAL	1	30	30	Potential.
CHAIN	31	689	659	MapN protein.

Sequence information

Length: 689 AA [This is the length of the unprocessed precursor]

Molecular weight: 76860 Da [This is the MW of the unprocessed precursor]

CRC64: CF88802B4F47C9CD [This is a checksum on the sequence]

10	20	30	40	50	60
MKFKSLITTT	LALGVLASTG	ANFNTNEASA	AAKQIDKSSS	SLHHGYSKIQ	IPYTITVNGT
70	80	90	100	110	120
SQNILSSLTF	NKNQQISYKD	IENKVKSPLY	FNRGISDIDL	RLSKQAKYTV	HFKNGTKRNV
130	140	150	160	170	180
DLKAGIHTAD	LINTSDIKAI	SVNVDTKKQV	KDKEAKANVQ	VPYTITVNGT	SQNILSNLTF
190	200	210	220	230	240
KKNQQISYKD	LENNVKSVLK	SNRGITDVDL	RLSKQAKFTV	NFKNGTKKVI	DLKAGIYTAN
250	260	270	280	290	300
LINTGDIKNI	NINVETKKQA	KDKEAKANNQ	VPYSINLNGT	TTNIQSNLAF	SNKPWTNYKN
310	320	330	340	350	360
LTAKVKSVLK	SDRGVSEEDL	KHAKKAYYTV	YFKNGGKRVV	HLNSNIYTAN	LVHAKDIKKI
370	380	390	400	410	420
EVTVKTGSKA	NAERYVPYTI	AVNGTSTPNL	SDLKFKGDSR	VSYSBITKKV	KSVLKYDRGI
430	440	450	460	470	480
GERELKYAKK	ATYTVHFKNG	TKKVINLNSK	ISQLNLLFVK	DIKKIDVDVK	TGSKAKADSY
490	500	510	520	530	540
VPYTIAVNGT	STPIASKLRL	SNKQLIGYQD	LNKKVKSVLK	HDRGINDIEL	KFAKQAKYTV

```

550      560      570      580      590      600
|       |       |       |       |       |
HFKNNGKTQVV DLKSDIFTRN LFSVKDIKKI DIDVKQHTKS NKALNKVANI ATKVKFPVTI

610      620      630      640      650      660
|       |       |       |       |       |
NGFSNVVSNE FAFLHPHKIT TNDLNAKLRL ALASDQGITK HDIGLSERTV YKVYFKDGSS

670      680
|       |
KFVDLKAQKQ DSKVFKATDI KKVDIEIKF
```

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[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),  
[Dotlet \(Java\)](#)




[ScanProsite](#), [MotifScan](#)



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Search   for

## Search in Swiss-Prot and TrEMBL for: mhcii

**Swiss-Prot Release 44.2 of 30-Jul-2004**

**TrEMBL Release 27.2 of 30-Jul-2004**

- 
- Number of sequences found in Swiss-Prot<sub>(0)</sub> and TrEMBL<sub>(7)</sub>: **7**
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  - For more directed searches, you can use the Sequence Retrieval System SRS.
- 

**Search in Swiss-Prot: There are matches to 0 out of 155596 entries**

---

**Search in TrEMBL: There are matches to 7 out of 1365262 entries**

### Q7ZYW1

SI:dZ194E12.12 (Novel MHCII beta chain protein) (Fragment) {GENE:Name=SI:dZ194E12.12} - Brachydanio rerio (Zebrafish) (Danio rerio)

### Q7ZYW2

SI:dZ194E12.11 (Novel MHCII alpha chain protein) {GENE:Name=SI:dZ194E12.11} - Brachydanio rerio (Zebrafish) (Danio rerio)

### Q7ZYW4

SI:dZ194E12.8 (Novel MHCII alpha chain protein) (Fragment) {GENE:Name=SI:dZ194E12.8} - Brachydanio rerio (Zebrafish) (Danio rerio)

### Q7ZYW5

SI:dZ194E12.7 (Novel MHCII beta chain protein ) (Fragment) {GENE:Name=SI:dZ194E12.7} - Brachydanio rerio (Zebrafish) (Danio rerio)

### Q801W0

SI:dZ266F07.2 (Novel MHCII alpha chain protein) {GENE:Name=SI:dZ266F07.2} - Brachydanio rerio (Zebrafish) (Danio rerio)

### Q9TPE3

MHC class II antigen (Fragment) {GENE:Name=MhcII} - Polypterus sp. (Bichir)

### Q9TPE4

MHC class II antigen (Fragment) {GENE:Name=MhcII} - Polypterus sp. (Bichir)

---

in Swiss-Prot/TrEMBL by AC, ID, description,  
gene name, organism

**Please do NOT use any boolean operators (and,  
or, etc.)**

---


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Format: ☒ Swiss-Prot ☐ Fasta

or

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Search <input type="text" value="Swiss-Prot/TrEMBL"/> <input type="button" value="Go"/> for <input type="text" value="mhci"/> <input type="button" value="Clear"/>				

# Search in Swiss-Prot and TrEMBL for: mhci

Swiss-Prot Release 44.2 of 30-Jul-2004  
TrEMBL Release 27.2 of 30-Jul-2004

- Number of sequences found in [Swiss-Prot](#)<sub>(0)</sub> and [TrEMBL](#)<sub>(7)</sub>: 7
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
- For more directed searches, you can use the Sequence Retrieval System [SRS](#).

Search in Swiss-Prot: There are matches to 0 out of 155596 entries

Search in TrEMBL: There are matches to 7 out of 1365262 entries

- [Q7ZYYW1](#) SI:dZ194E12.12 (Novel MHCII beta chain protein) (Fragment) {GENE:Name=SI:dZ194E12.12} - Brachydanio rerio (Zebrafish)  
(Danio rerio)
- [Q7ZYYW2](#) SI:dZ194E12.11 (Novel MHCII alpha chain protein) {GENE:Name=SI:dZ194E12.11} - Brachydanio rerio (Zebrafish) (Danio rerio)
- [Q7ZYYW4](#) SI:dZ194E12.8 (Novel MHCII alpha chain protein) (Fragment) {GENE:Name=SI:dZ194E12.8} - Brachydanio rerio (Zebrafish) (Danio rerio)
- [Q7ZYYW5](#)

SI:dZ194E12.7 (Novel MHCII beta chain protein ) (Fragment) {GENE:Name=SI:dZ194E12.7} - Brachydanio rerio (Zebrafish) (Danio rerio)  
Q801W0  
SI:dZ266F07.2 (Novel MHCII alpha chain protein) {GENE:Name=SI:dZ266F07.2} - Brachydanio rerio (Zebrafish) (Danio rerio)  
Q9TPE3  
MHC class II antigen (Fragment) {GENE:Name=MhclI} - Polypterus sp. (Bichir)  
Q9TPE4  
MHC class II antigen (Fragment) {GENE:Name=MhclI} - Polypterus sp. (Bichir)

 New Search

in Swiss-Prot/TrEMBL by AC, ID, description, gene name, organism  
**Please do NOT use any boolean operators (and, or, etc.)**

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## Entry information

Entry name **CNA\_STAAU**

Primary accession number **Q53654**

Secondary accession numbers None

Entered in Swiss-Prot in Release 37, December 1998

Sequence was last modified in Release 37, December 1998

Annotations were last modified in Release 45, October 2004

## Name and origin of the protein

Protein name **Collagen adhesin [Precursor]**

Synonyms None

Gene name **Name: cna**

From **Staphylococcus aureus [TaxID: 1280]**

Taxonomy **Bacteria; Firmicutes; Bacillales; Staphylococcus.**

## References

- [1] SEQUENCE FROM NUCLEIC ACID.  
**STRAIN=FDA 574;**  
 MEDLINE=92165839;PubMed=1311320 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel, Japan](#)]  
[Patti J.M.](#), [Jonsson H.](#), [Guss B.](#), [Switalski L.M.](#), [Wiberg K.](#), [Lindberg M.](#), [Hoeoek M.](#);  
 "Molecular characterization and expression of a gene encoding a Staphylococcus aureus collagen adhesin."; [J. Biol. Chem. 267:4766-4772\(1992\)](#).
- [2] ERRATUM.  
[Patti J.M.](#), [Jonsson H.](#), [Guss B.](#), [Switalski L.M.](#), [Wiberg K.](#), [Lindberg M.](#), [Hoeoek M.](#);  
[J. Biol. Chem. 269:11672-11672\(1994\)](#).

[3] COLLAGEN-BINDING DOMAIN.

**STRAIN**=FDA 574;

**MEDLINE**=94032261;PubMed=8218209 [[NCBI](#), [ExpASY](#), [EBI](#), [Israel](#), [Japan](#)]

[Patti J.M.](#), [Boles J.O.](#), [Hoeoek M.](#);

"Identification and biochemical characterization of the ligand binding domain of the collagen adhesin from *Staphylococcus aureus*."; [Biochemistry](#) 32:11428-11435(1993).

[4] X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 169-318.

**MEDLINE**=97475225;PubMed=9334749 [[NCBI](#), [ExpASY](#), [EBI](#), [Israel](#), [Japan](#)]

[Symersky J.](#), [Patti J.M.](#), [Carson M.](#), [House-Pompeo K.](#), [Teale M.](#), [Moore D.](#), [Jin L.](#), [Schneider A.](#), [DeLucas L.J.](#), [Hoeoek M.](#), [Narayana S.V.L.](#);

"Structure of the collagen-binding domain from a *Staphylococcus aureus* adhesin. ";

[Nat. Struct. Biol.](#) 4:833-838(1997).

**Comments**

- **FUNCTION:** Mediates attachment of staphyococcal cells to collagen-containing substrata.
- **SUBCELLULAR LOCATION:** Attached to the cell wall peptidoglycan by an amide bond (*Potential*).

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**Cross-references**

**EMBL**

[M81736](#); [AAA20874.1](#); - [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]

[1AMX](#); [24-JUN-98](#). [[ExpASY](#) / [RCSB](#) / [EBI](#)]

[1D2O](#); [27-SEP-00](#). [[ExpASY](#) / [RCSB](#) / [EBI](#)]

[1D2P](#); [27-SEP-00](#). [[ExpASY](#) / [RCSB](#) / [EBI](#)]

[Detailed list of linked structures.](#)

[IPR008966](#); [Adhes\\_bact.](#)

[IPR008454](#); [Cna\\_B.](#)

[IPR008970](#); [Cna\\_B\\_unit.](#)

[IPR008456](#); [Collagen\\_bind.](#)

[IPR001899](#); [Gram\\_pos\\_anchor.](#)

[Graphical view of domain structure.](#)

[PF05738](#); [Cna\\_B; 7.](#)

[PF05737](#); [Collagen\\_bind; 1.](#)

[Pfam graphical view of domain structure.](#)

[TIGR01167](#); [LPXTG\\_anchor; 1.](#)

**TIGRFAMs**

[PS50847](#); [GRAM\\_POS\\_ANCHORING](#); [FALSE\\_NEG.](#)

PROSITE graphical view of domain structure.

[Domain structure / List of seq. sharing at least 1 domain]

[Family / Alignment / Tree]

Q53654.

Q53654.

Q53654.

Q53654.

053654.

053654.

O53654: B6A1CC072E575D76.

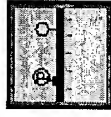
Get region on 2D PAGE.

View cluster of proteins with at least 50% / 90% identity.

## Keywords

**3D-structure; Cell wall; Peptidoglycan-anchor; Repeat; Signal.**

## Features



### Feature table viewer



## Feature aligner

Key	From	To	Length	Description
SIGNAL	<u>1</u>	<u>29</u>	29	Potential.
CHAIN	<u>30</u>	<u>1154</u>	1125	Collagen adhesin.
PROPEP	<u>1155</u>	<u>1183</u>	29	Removed by sortase (Potential).
DOMAIN	<u>151</u>	<u>318</u>	168	Collagen-binding.
DOMAIN	<u>533</u>	<u>1093</u>	561	3 X 187 AA approximate tandem repeats.
DOMAIN	<u>1093</u>	<u>1157</u>	65	Lys/Pro-rich; cell wall-spanning.
REPEAT	<u>533</u>	<u>719</u>	187	B1.
REPEAT	<u>720</u>	<u>906</u>	187	B2.
REPEAT	<u>907</u>	<u>1093</u>	187	B3.
SITE	<u>1151</u>	<u>1155</u>	5	LPXTG sorting signal (Potential).
MOD_RES	<u>1154</u>	<u>1154</u>		Pentaglycyl murein peptidoglycan amidated threonine (Potential).
STRAND	<u>174</u>	<u>179</u>	6	
TURN	<u>182</u>	<u>183</u>	2	
TURN	<u>185</u>	<u>186</u>	2	

STRAND	<u>187</u>	<u>194</u>	8
TURN	<u>196</u>	<u>197</u>	2
STRAND	<u>201</u>	<u>201</u>	1
STRAND	<u>205</u>	<u>211</u>	7
STRAND	<u>215</u>	<u>228</u>	14
TURN	<u>229</u>	<u>230</u>	2
STRAND	<u>232</u>	<u>234</u>	3
HELIX	<u>239</u>	<u>246</u>	8
TURN	<u>248</u>	<u>249</u>	2
STRAND	<u>251</u>	<u>255</u>	5
TURN	<u>256</u>	<u>259</u>	4
STRAND	<u>260</u>	<u>265</u>	6
HELIX	<u>267</u>	<u>270</u>	4
TURN	<u>271</u>	<u>272</u>	2
STRAND	<u>273</u>	<u>283</u>	11
TURN	<u>286</u>	<u>287</u>	2
STRAND	<u>290</u>	<u>299</u>	10
STRAND	<u>301</u>	<u>301</u>	1
TURN	<u>302</u>	<u>303</u>	2
STRAND	<u>307</u>	<u>311</u>	5
STRAND	<u>314</u>	<u>317</u>	4
STRAND	<u>534</u>	<u>544</u>	11
TURN	<u>546</u>	<u>550</u>	5
STRAND	<u>556</u>	<u>563</u>	8
TURN	<u>564</u>	<u>565</u>	2
STRAND	<u>566</u>	<u>574</u>	9
HELIX	<u>575</u>	<u>577</u>	3
TURN	<u>578</u>	<u>579</u>	2
STRAND	<u>580</u>	<u>587</u>	8
STRAND	<u>589</u>	<u>590</u>	2
TURN	<u>591</u>	<u>592</u>	2
STRAND	<u>593</u>	<u>594</u>	2
STRAND	<u>597</u>	<u>601</u>	5
TURN	<u>605</u>	<u>606</u>	2
STRAND	<u>607</u>	<u>612</u>	6



TURN	613	614	2
STRAND	615	620	6
TURN	622	623	2
STRAND	624	634	11
TURN	636	640	5
STRAND	646	653	8
TURN	654	655	2
STRAND	656	665	10
HELIX	666	668	3
TURN	669	670	2
STRAND	671	678	8
STRAND	680	680	1
STRAND	685	685	1
STRAND	688	692	5
TURN	697	698	2
STRAND	700	704	5
TURN	708	709	2
STRAND	711	716	6
STRAND	721	731	11
TURN	733	737	5
STRAND	744	750	7
TURN	751	752	2
STRAND	753	760	8
HELIX	762	764	3
TURN	765	765	1
STRAND	767	774	8
STRAND	776	777	2
TURN	778	779	2
STRAND	780	781	2
STRAND	784	788	5
TURN	792	793	2
STRAND	794	799	6
TURN	800	801	2
STRAND	802	807	6
TURN	809	810	2



STRAND	<u>811</u>	<u>821</u>	11
HELIX	<u>823</u>	<u>825</u>	3
TURN	<u>826</u>	<u>827</u>	2
STRAND	<u>833</u>	<u>840</u>	8
TURN	<u>841</u>	<u>842</u>	2
STRAND	<u>843</u>	<u>852</u>	10
TURN	<u>853</u>	<u>857</u>	5
STRAND	<u>858</u>	<u>865</u>	8
STRAND	<u>867</u>	<u>868</u>	2
TURN	<u>869</u>	<u>870</u>	2
STRAND	<u>871</u>	<u>872</u>	2
STRAND	<u>875</u>	<u>879</u>	5
TURN	<u>884</u>	<u>885</u>	2
STRAND	<u>886</u>	<u>891</u>	6
HELIX	<u>895</u>	<u>897</u>	3
STRAND	<u>898</u>	<u>904</u>	7

Sequence information

Length: **1183 AA** [This is the length of the unprocessed precursor]      Molecular weight: **133066 Da** [This is the MW of the unprocessed precursor]      CRC64: **B6A1CC072E575D76** [This is a checksum on the sequence]

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70		80	90	100	110	120
DDKNGKIQNG	DMIKVAVPTS	GTVKIEGYSK	TVPLTVKGEQ	VGQAVITPDG	ATITFNDKVE	
130		140	150	160	170	180
KLSDVSGFAE	FEVQGRNLTQ	TNTSDDKVAT	ITSGNKSTNV	TVHKSEAGTS	SVFYKYKTGDM	
190		200	210	220	230	240
LPEDTTHVRW	FLNINNEKSY	VSKDITIKDQ	IQGGQQLDLS	TLNINVTGTH	SNYYSGQSAI	
250		260	270	280	290	300
TDFEKAFPGS	KITVDNTKNT	IDVTIPQGYG	SYNSFSINYK	TKITNEQQKE	FVNNSQAWYQ	

310		320		330		340		350		360
EHGKEEVNGK	SNHHTVHNIN	ANAGIEGTVK	GELKVLKQDK	DTKAPIANVK	FKLSKKDGSV					
370		380		390		400		410		420
VKDNQKEIEI	ITDANGIANI	KALPSGDYIL	KEIEAPRPYT	FDKDKKEYPFT	MKDTDNQGYF					
430		440		450		460		470		480
TTIENAKAIE	KTKDVSQAQV	WEGTQVKVKT	IYFKLYKQDD	NQNTTPVDKA	EIKKLEDGTT					
490		500		510		520		530		540
KVTVSNLPEN	DKNGKAIKYL	VKEVNAQGED	TTPEGYTKKE	NGLVVTNTEK	PIETTTSISGE					
550		560		570		580		590		600
KWDDDKDNQD	GKRPEKVSVN	LLANGEKVKT	LDVTSETNWK	YEFKDLPKYD	EGKKIEYTVT					
610		620		630		640		650		660
EDHVKDYTTD	INGTTITNKY	TPGETSATVT	KNWDDNNNQD	GKRPTTEIKVE	LYQDGKATGK					
670		680		690		700		710		720
TAILNESNNW	THTWTGLDEK	AKGQQVKYTV	EELTKVKGYT	THVDNNDMGN	LIVTNKYTPE					
730		740		750		760		770		780
TTSISGEKVW	DDKDNQDGKR	PEKVSVNLLA	DGEKVKTLDV	TSETNWKYEF	KDLPKYDEGK					
790		800		810		820		830		840
KIEYTVTEDH	VKDYTTDDING	TTITNKYTPG	ETSATVTKNW	DDNNNQDGKR	PTEIKVELYQ					
850		860		870		880		890		900
DGKATGKTAI	LNESNNWTHT	WTGLDEKAKG	QQVKYTVVEEL	TKVKGYTTHV	DNNDMGNLIV					
910		920		930		940		950		960
TNKYTPETTS	ISGEKVWDDK	DNQDGKRPEK	VSVNLLANGE	KVKTLDDVTSE	TNWKYEFKDL					

970 980 990 1000 1010 1020  
| | | | |  
PKYDEGKKIE YTVTEDHVKD YTTDINGTTI TNKYTPGETS ATVTKNWDDN NNQDGKRPT  
1030 1040 1050 1060 1070 1080  
| | | | |  
IKVELYQDGK ATGKTAILNE SNNWTHWTG LDEKAKGQQV KYTVDELTKV NGYTTTHVDNN  
1090 1100 1110 1120 1130 1140  
| | | | |  
DMGNLIVTNK YTPKKPNKPI YPEKPKDKTP PTKPDHSNKV KPTPPDKPSK VDKDDQPKDN  
1150 1160 1170 1180  
| | | |  
KTKPENPLKE LPKTGMKIIT SWITWVFIGI LGLYLILRKR FNS

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None

Cross-references

EMBL BX571856; CAG41749.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]  
ProDom [Domain structure / List of seq. sharing at least 1 domain]  
HOBACGEN [Family / Alignment / Tree]  
ProtoMap Q6GDB2.  
PRESAGE Q6GDB2.  
ModBase Q6GDB2.  
SMR Q6GDB2; 24FB7F7244D42C34.  
SWISS-2DPAGE Get region on 2D PAGE.  
UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Collagen.

Features

None

Sequence information

Length: 1183 AA    Molecular weight: 133048 Da    CRC64: 24FB7F7244D42C34 [This is a checksum on the sequence]

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70		80		90		100		110		120	
DDKNGKIQNG	DTIKVAVPTS	GTVKIEGYSK	TVSLTVKGEQ	VGQAVITPDG	ATITFNDKVE						
130		140		150		160		170		180	
KLSDVSGFAE	FEVQGRNLTQ	TNTSDDKVAT	ITSGNKSTNV	TVHKSEAGTS	SVFYKKTGDM						
190		200		210		220		230		240	
LPEDTTHVRW	FLNINNEKRY	VSKDITIKDQ	IQQGQQLDLS	TLNINVTGTH	SNYYSGPNAI						
250		260		270		280		290		300	
TDFEKAPPGS	KITVDNTKNT	IDVTIPQGYG	SLNSFSINYK	TKITNEQQKE	FVNNSQAWYQ						

310		320		330		340		350		360	
EHGKEEVNGK	AFNHTVHNIN	ANAGIEGTVK	GELKVLKQDK	DTKAPIANVK	FKLSKKDGSV						
370		380		390		400		410		420	
VKDNQKEIEI	KTDANGIANI	KALPSGDYIL	KEIEAPAPYT	FDKKEYPFT	MKDTDNQGYF						
430		440		450		460		470		480	
TTIENAKEIE	KTKDVSAQKV	WEGTQVKVPT	IYFKLYKQDD	NQNTTPVDKA	EIKKLEDGTT						
490		500		510		520		530		540	
KVTWSNLPEN	DNKGKTIKYL	VKEVNAQGKD	TTPEGYTKKE	DGLVVTNTEK	PIETTSISGE						
550		560		570		580		590		600	
KVWDDKDNQD	GKRPEKVSVN	LLANGEKVET	VDVTSETNWK	YKFKDLPKYD	EGKKIEYTVT						
610		620		630		640		650		660	
EDHVKDYYTD	INGTTITNKY	TPGETSATVT	KNWDDNNNQD	GKRPTKIVE	LYQDGKATGK						
670		680		690		700		710		720	
TATLINESNNW	THTWTGLDEK	AKGQQVKYTV	EELTKVKGYT	THVDNNDMGN	LIVTNKYTPE						
730		740		750		760		770		780	
TTSISGEKVW	DDKDNQDGKR	PEKVSVNLLA	NGEKVKTLDV	TSETNWKYEF	KDLPKYDEGK						
790		800		810		820		830		840	
KIEYTVTEDH	VKDYTTDING	TTITNKYTPG	ETSATVTKNW	DDNNNQDGKR	PTEIKVELYQ						
850		860		870		880		890		900	
DGKATVKTAT	LNESNNWTHT	WTGLDEKAKG	QQVKYTVVEEL	TKVKGYTTHV	DNNDMGNLIV						
910		920		930		940		950		960	
TNKYTPETTS	ISGEKVWDDK	DNQDGKRPEK	VSVNLLANGE	KVKTLDDVTSE	TNWKYEFKNL						

970 | 980 990 1000 1010 1020  
PKYDEGKKIE YTVTEDHVKD YTTDINGTTI TNKYTPGETS ATVTKNWDDN NNQDGKRPT  
1030 | 1040 1050 1060 1070 1080  
IKVELYQDGK ATGKTATLNE SNNWTHWTG LDEKAKGQQV KYTVEELTKV NGYTTHVDNN  
1090 | 1100 1110 1120 1130 1140  
DMGNLIVTNK YTPEKPNKPI YPEKPKDKTP PTKPDHSNKV KPTPPDKPSK VDKDDQPKDN  
1150 | 1160 1170 1180  
KTKPENPLKE LPKTGMKIIT SWITWVFIGI LGLYLILRKR FNS

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## Entry information

**Entry name** **Q53630**  
**Primary accession number** **Q53630**  
**Secondary accession numbers** None  
**Entered in TrEMBL in** Release 01, November 1996  
**Sequence was last modified in** Release 18, October 2001  
**Annotations were last modified in** Release 24, June 2003

## Name and origin of the protein

**Protein name** **Cell surface elastin binding protein**  
**Synonyms** None  
**Gene name** **Name: ebpS**  
**From** Staphylococcus aureus [TaxID: 1280]  
**Taxonomy** Bacteria; Firmicutes; Bacillales; Staphylococcus.

## References

- [1] SEQUENCE FROM NUCLEIC ACID.  
**STRAIN**=ATCC 12598;  
MEDLINE=96279109;PubMed=8663124 [NCBI, ExPASy, EBI, Israel, Japan]  
Park P.W., Rosenbloom J., Abrams W.R., Rosenbloom J., Mechem R.P.;  
"Molecular cloning and expression of the gene for elastin-binding protein (ebpS) in Staphylococcus aureus."; J. Biol. Chem. 271:15803-15809(1996).
- [2] SEQUENCE FROM NUCLEIC ACID.  
**STRAIN**=ATCC 12598;  
MEDLINE=21634882;PubMed=11684686 [NCBI, ExPASy, EBI, Israel, Japan]

Downer R., Roche F., Park P.W., Mecham R.P., Foster T.J.;  
 "The elastin-binding protein of Staphylococcus aureus (EbpS) is expressed at the cell surface as an integral membrane protein and not as a cell-wall associated protein.";  
 J. Biol. Chem. 277:243-250(2002).  
 [3] SEQUENCE FROM NUCLEIC ACID.  
 STRAIN=ATCC 12598;  
 Roche F.M., Foster T.J.;  
 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL

U48826; AAC44135.2; -.[\[EMBL / GenBank / DDBJ\]](#) [\[CoDingSequence\]](#)

GO

[GO:0016998](#); Biological process: cell wall catabolism (*inferred from electronic annotation*).

InterPro

[IPR002482](#); LysM.

[Graphical view of domain structure](#).

Pfam

[PF01476](#); LysM; 1.

[Pfam graphical view of domain structure](#).

SMART

[SM00257](#); LysM; 1.

ProDom

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HOBACGEN

[\[Family / Alignment / Tree\]](#)

ProtoMap

[Q53630](#).

PRESAGE

[Q53630](#).

ModBase

[Q53630](#).

SMR

[Q53630](#); 62904CF86C1F56B8.

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Keywords

None

Features

None

Sequence information

Length: **486 AA**    Molecular weight: **53080 Da**    **CRC64: 62904CF86C1F56B8** [This is a checksum on the sequence]

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70	80	90	100	110	120
DLATNHNKQV	HNESQTSEDN	VQNEAGTIDD	QVESHSHSTE	SQEPHQDST	PQHEEGYYNK
130	140	150	160	170	180
NAFAMDKSHP	EPIEDNDKHE	TIKEAENNTE	HSTVSDKSEA	EQSQQPKPYF	ATGANQANTS
190	200	210	220	230	240
KDKHDDVTVK	QDKDESKDHH	SGKKGAAIGA	GTAGVAGAAG	AMGVSKAKKH	SNDAQNKSNS
250	260	270	280	290	300
GKVNNSTEDK	ASEDKSKEHH	NGKKGAAIGA	GTAGLAGGAA	SNSASAASKP	HASNNASQNN
310	320	330	340	350	360
DEHDHHRDK	ERKKGGMAKV	LLPLIAAVLI	IGALAIFGGM	ALNNHNNGTK	ENKIAINTNKN
370	380	390	400	410	420
NADESKDKDT	SKDASKDKSK	STSDSKSKDD	QDKATKDESD	NDQNNANQAN	NQAQNNQNQQ
430	440	450	460	470	480
QANQNQQQQQ	QRQGGGQRHT	VNGQENLYRI	AIQYYGSGSP	ENVEKIRРАН	GLSGNNIRNG

QQIVIP

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or at [NCBI \(USA\)](#)

[PeptideMass](#), [PeptideCutter](#), [Dotlet](#) (Java)




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TrEMBL: Q6GGT1**

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## Entry information

Entry name	<b>Q6GGT1</b>
Primary accession number	<b>Q6GGT1</b>
Secondary accession numbers	None
Entered in TrEMBL in	Release 28, October 2004
Sequence was last modified in	Release 28, October 2004
Annotations were last modified in	Release 28, October 2004

## Name and origin of the protein

Protein name	Cell surface elastin binding protein
Synonyms	None

Gene name	Name: ebpS
	ORFNames: SAR1489

From Staphylococcus aureus subsp. aureus MRSA252 [TaxID: 282458]

**Taxonomy**  
Bacteria; Firmicutes; Bacillales; Staphylococcus.

## References

[1] SEQUENCE FROM NUCLEIC ACID.

**STRAIN=MRSA252;**

Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabinowitsch E., Rutherford K., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J.;

"Complete genomes of two clinical *Staphylococcus aureus* strains: evidence for the rapid evolution of virulence and drug resistance."; Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

None

Cross-references

EMBL BX571856; CAG40487.1; -[[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]

ProDom [Domain structure / List of seq. sharing at least 1 domain]

HOBACGEN [[Family](#) / [Alignment](#) / [Tree](#)]

ProtoMap [Q6GGT1](#).

PRESAGE [Q6GGT1](#).

ModBase [Q6GGT1](#).

SMR [Q6GGT1](#); 62904CF86C1F56B8.

SWISS-2DPAGE [Get region on 2D PAGE](#).

UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

None

Features

None

Sequence information

Length: 486 AA Molecular weight: 53080 Da CRC64: 62904CF86C1F56B8 [This is a checksum on the sequence]

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MSNNFKDDFE	KNRQSIDTNS	HQDHTEDVEK	DQSELEHQDT	IENTEQQFPP	RNAQRRKRRR					
70		80		90		100		110		120
DLATNHNKQV	HNESQTSEDN	VQNEAGTIDD	RQVESSHSTE	SQEPSHQDST	PQHEEGYYNK					
130		140		150		160		170		180
NAFAMDKSHP	EPIEDNDKHE	TIKEAENNTE	HSTVSDKSEA	EQSQQPKPYF	ATGANQANTS					
190		200		210		220		230		240
KDKHDDVTVK	QDKDESKDHH	SGKKGAAIGA	GTAGVAGAAG	AMGVSKAKKH	SNDAQNKSNS					
250		260		270		280		290		300
GKVNNSTEDK	ASEDKSKEHH	NGKKGAAIGA	GTAGLAGGAA	SNSASAASKP	HASNNASQNN					

310	320	330	340	350	360
DEHDDHDDK	ERKKGGMAKV	LLPLIAAVLI	IGALAIFGGM	ALNNHNGTK	ENKIANTNKN
370	380	390	400	410	420
NADESKDKDT	SKDASKDKSK	STSDSKSKDD	QDKATKDESD	NDQNNANQAN	NQAQNNQNQQ
430	440	450	460	470	480
QANQNQQQQQ	QRQGGGQRHT	VNGQENLYRI	AIQYYGSGSP	ENVEKIRRAN	GLSGNNIRNG

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**TrEMBL: Q7A5I6**

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## Entry information

Entry name	<b>Q7A5I6</b>
Primary accession number	<b>Q7A5I6</b>
Secondary accession numbers	None
Entered in TrEMBL in	Release 27, July 2004
Sequence was last modified in	Release 27, July 2004
Annotations were last modified in	Release 27, July 2004

## Name and origin of the protein

Protein name	<b>Elastin binding protein</b>
Synonyms	None
Gene name	<b>Name: ebpS</b>
From	<u>Staphylococcus aureus (strain N315)</u> [TaxID: 158879]
Taxonomy	<u>Bacteria; Firmicutes; Bacillales; Staphylococcus.</u>

## References

[1] SEQUENCE FROM NUCLEIC ACID.

**STRAIN=N315:**

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K., Nagai Y., Lian J., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R., Kaïto C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*." ; Lancet 357:1225-1240(2001).

[2]



STRAIN=N315;  
Director-General, [Biotechnology Center](#), [Aoki K.](#), [Oguchi A.](#), [Hosoyama A.](#), [Nagai Y.](#), [Kuroda M.](#), [Hiramatsu K.](#), [Kikuchi H.](#);  
Submitted (JAN-2001) to the [EMBL/GenBank/DBJ](#) databases.

Comments

None

Cross-references

EMBL [AP003134](#); [BAB42574.1](#); -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]  
ProDom [\[Domain structure / List of seq. sharing at least 1 domain\]](#)  
HOBACGEN [\[Family / Alignment / Tree\]](#)  
ProtoMap [Q7A5I6](#).  
PRESAGE [Q7A5I6](#).  
ModBase [Q7A5I6](#).  
SMR [Q7A5I6](#); [F4DA049456C09A36](#).  
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UniRef [View cluster of proteins with at least 50% / 90% identity](#).

Keywords

None

Features

None

Sequence information

Length: 486 AA    Molecular weight: 53181 Da    CRC64: [F4DA049456C09A36](#) [This is a checksum on the sequence]

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130	140	150	160	170	180
NAFAMDKSHP	EPIEDNDKHE	TIKDAENNTE	HSTVSDKSIA	EQSQQPKPYF	ATGANQANTS
190	200	210	220	230	240
KDKHDDVTVK	QDKDESKDHH	SGKKGAAIGA	GTAGVAGAAG	AMGVSKAKKH	SNDAQNKSNS

250 | 260 270 280 290 300  
DKSNNSTEDK ASQDKSKDHH NGKKGAAIGA GTAGLAGGAA SKSASAASKP HASNNASQNH  
310 | 320 330 340 350 360  
DEHDNHDRDK ERKKGGMKV LLPLIAAVLI IGALAIFGGM ALNNHNNGTK ENKIANTNKN  
370 | 380 390 400 410 420  
NADESKDKT SKDASKDKSK STSDSKSKED QDKATKDESD NDQNNANQAN NQAQNNQNQQ  
430 | 440 450 460 470 480  
QANQNQQQQQ QRQGGGQRHT VNGQENLYRI AIQYYGSGSP ENVEKIRРАН GLSGNNIRNG

QQIVIP

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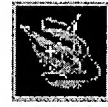
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## TrEMBL: Q8NWM5

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### Entry information

Entry name **Q8NWM5**  
 Primary accession number **Q8NWM5**  
 Secondary accession numbers None  
 Entered in TrEMBL in Release 22, October 2002  
 Sequence was last modified in Release 22, October 2002  
 Annotations were last modified in Release 26, March 2004

### Name and origin of the protein

Protein name **Elastin binding protein**  
 Synonyms None  
 Gene name **Name: ebpS**  
 From **Staphylococcus aureus (strain MW2) [TaxID: 196620]**  
 Taxonomy **Bacteria; Firmicutes; Bacillales; Staphylococcus.**

### References

[1] SEQUENCE FROM NUCLEIC ACID.  
**STRAIN=**MW2;  
 MEDLINE=22040717;PubMed=12044378 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]  
[Baba T.](#), [Takeuchi F.](#), [Kuroda M.](#), [Yuzawa H.](#), [Aoki K.-I.](#), [Oguchi A.](#), [Nagai Y.](#), [Iwama N.](#), [Asano K.](#), [Naimi T.](#), [Kuroda H.](#), [Cui L.](#),  
[Yamamoto K.](#), [Hiramatsu K.](#);  
 "Genome and virulence determinants of high virulence community-acquired MRSA.";  
 Lancet 359:1819-1827(2002).

### Comments

None

Cross-references

EMBL AP004827; BAB95234.1; -.[\[EMBL / GenBank / DDBJ\]](#) [\[CoDingSequence\]](#)  
GO [GO:0016998](#); Biological process: cell wall catabolism (*inferred from electronic annotation*).  
CMR [Q8NWM5](#); [Q8NWM5](#).  
InterPro [IPR002482](#); LysM.  
Pfam [PF01476](#); LysM; 1.  
SMART [SM00257](#); LysM; 1.  
ProDom [\[Domain structure / List of seq. sharing at least 1 domain\]](#)  
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ModBase [Q8NWM5](#).  
SMR [Q8NWM5](#); 8859F271713E7218.  
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UniRef [View cluster of proteins with at least 50% / 90% identity](#).

Keywords

Complete proteome.

Features

None

Sequence information

Length: 486 AA    Molecular weight: 53239 Da    CRC64: 8859F271713E7218 [This is a checksum on the sequence]

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70	80	90	100	110	120
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130	140	150	160	170	180
NAFAMDKSHP	EPIEDNDKHE	TIKEAENNTE	HSTVSDKSEA	EQSQQPKPYF	ATGANQANTS

190 | 200 | 210 | 220 | 230 | 240  
KDKHDDVTVK QDKDESKDHH SGKKGAAIGA GTAGVAGAAG AMGVSKAKKH SND AQNKSNS  
250 | 260 | 270 | 280 | 290 | 300  
DKSNNSTEDK VSQDKSKDHH NGKKGAAIGA GTAGLAGGAA SKSASAASKP HASNNASQNH  
310 | 320 | 330 | 340 | 350 | 360  
DEHDNHRDCK ERKKGGMAKV LLPLIAAVLI IGALAIFGGM ALNNHNNGTG ENK IANTNKN  
370 | 380 | 390 | 400 | 410 | 420  
NADESKDKT SKDASKDKSK STSDSKSKED QDKATKDESD NDQNNANQAN NQAQNNQNQQ  
430 | 440 | 450 | 460 | 470 | 480  
QANQNQQQQQ QROGGGQRHT VNGQENLYRI AIQYYGSGSP ENVEKIRRAN GLSGNNIRNG

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## TrEMBL: Q93D59

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### Entry information

Entry name **Q93D59**  
 Primary accession number **Q93D59**  
 Secondary accession numbers None  
 Entered in TrEMBL in Release 19, December 2001  
 Sequence was last modified in Release 19, December 2001  
 Annotations were last modified in Release 24, June 2003

### Name and origin of the protein

Protein name **Cell surface elastin binding protein EbpS**  
 Synonyms None  
 Gene name **Name: ebpS**  
 From Staphylococcus aureus [TaxID: 1280]  
 Taxonomy Bacteria; Firmicutes; Bacillales; Staphylococcus.

### References

[1] SEQUENCE FROM NUCLEIC ACID.

**STRAIN**=8325-4;  
 MEDLINE=21634882;PubMed=11684686 [[NCBI](#), [ExPASy](#), [EBL](#), [Israel, Japan](#)]  
[Downer R.](#), [Roche F.](#), [Park P.W.](#), [Mecham R.P.](#), [Foster T.J.](#);  
 "The elastin-binding protein of *Staphylococcus aureus* (EbpS) is expressed at the cell surface as an integral membrane protein and not as a cell-wall associated protein."  
[J. Biol. Chem.](#) 277:243-250(2002).

[2] SEQUENCE FROM NUCLEIC ACID.

**STRAIN**=8325-4;

Roche F.M., Foster T.J.;  
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL

AF400161; AAL00934.1; -.[[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]

GO

GO:0016998;Biological process: cell wall catabolism (*inferred from electronic annotation*).

InterPro

[IPR002482](#); LysM.

[Graphical view of domain structure](#).

Pfam

[PF01476](#); LysM; 1.

[Pfam graphical view of domain structure](#).

SMART

[SM00257](#); LysM; 1.

ProDom

[\[Domain structure / List of seq. sharing at least 1 domain\]](#)

HOBACGEN

[\[Family / Alignment / Tree\]](#)

ProtoMap

[Q93D59](#).

PRESAGE

[Q93D59](#).

ModBase

[Q93D59](#).

SMR

[Q93D59](#); 70173FD572F47AD8.

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Keywords

None

Features

None

Sequence information

Length: 486 AA    Molecular weight: 53221 Da    CRC64: 70173FD572F47AD8 [This is a checksum on the sequence]

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70	80	90	100	110	120
DLATNHNKQV	HNESQTSEDN	VQNEAGTIDD	RQVESSHSTE	SQEPHQDST	PQHEEYYNK

130		140	150	160	170	180																																													
NAFAMDKSH	P	E	I	E	D	N	D	K	H	T	I	K	N	A	E	N	N	T	E	H	S	T	V	S	D	K	S	E	A	E	Q	S	Q	P	K	P	Y	F	T	T	G	A	N	Q	S	E	T	S			
190		200	210	220	230	240																																													
KNEHDNDSV	K	Q	D	E	P	K	E	H	H	N	G	K	K	A	A	A	I	G	A	G	T	A	G	V	A	G	A	A	M	A	A	S	K	A	K	K	H	S	N	D	A	Q	N	K	S	N	S				
250		260	270	280	290	300																																													
GKANNSTED	K	A	S	Q	D	K	S	K	D	H	H	N	G	K	K	G	A	A	I	G	A	G	T	A	G	L	A	G	G	A	A	S	K	S	A	S	A	A	S	K	P	H	A	S	N	N	A	S	Q	N	H
310		320	330	340	350	360																																													
DEHDNHRDK	E	R	K	K	G	G	M	A	K	V	L	L	P	L	I	A	A	V	L	I	I	G	A	L	A	I	F	G	G	M	A	L	N	N	H	N	G	T	K	E	N	K	I	A	N	T	N	K	N		
370		380	390	400	410	420																																													
NADESKDKT	S	K	D	A	S	K	D	K	S	K	E	D	S	T	D	S	D	K	S	K	E	D	Q	D	K	A	T	K	D	E	S	D	N	Q	N	N	A	N	Q	A	N	Q	N	N	Q	Q					
430		440	450	460	470	480																																													
QANQNQQQQ	Q	Q	R	Q	G	G	Q	R	H	T	V	N	Q	E	N	L	Y	R	I	A	I	Q	Y	Y	G	S	G	S	P	E	N	V	E	K	I	R	R	A	N	G	L	S	G	N	N	I	R	N	G		

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US 20040101919A1

(19) **United States**

(12) **Patent Application Publication** (10) **Pub. No.: US 2004/0101919 A1**

**Hook et al.** (43) **Pub. Date: May 27, 2004**

(54) **BIOINFORMATIC METHOD FOR IDENTIFYING SURFACE-ANCHORED PROTEINS FROM GRAM-POSITIVE BACTERIA AND PROTEINS OBTAINED THEREBY**

**Related U.S. Application Data**

(60) Provisional application No. 60/410,303, filed on Sep. 13, 2002.

**Publication Classification**

(51) **Int. Cl.<sup>7</sup>** ..... G01N 33/554; G01N 33/569  
(52) **U.S. Cl.** ..... 435/7.32

(76) **Inventors:** Magnus Hook, Houston, TX (US); Yi Xu, Houston, TX (US); Jouko V. Sillanpaa, Houston, TX (US); Narayana Sthanam, Birmingham, AL (US); Karthe Ponnuraj, Birmingham, AL (US); Joseph M. Patti, Cumming, GA (US); Jeff T. Hutchins, Cumming, GA (US); Andrea Hall, Acworth, GA (US); Maria G. Bowden, Sugarland, TX (US)

**Correspondence Address:**

**STITES & HARBISON PLLC  
1199 NORTH FAIRFAX STREET  
SUITE 900  
ALEXANDRIA, VA 22314 (US)**

(21) **Appl. No.: 10/661,809**

(22) **Filed: Sep. 15, 2003**

**ABSTRACT**

A bioinformatic method is provided for identifying and isolating proteins with MSCRAMM®-like characteristics from Gram positive bacteria, such as Enterococcus, Staphylococcus, Streptococcus and Bacillus bacteria, which can then be utilized in methods to prevent and treat infections caused by Gram-positive bacteria. The method involves identifying from sequence information those proteins with a putative C-terminal LPXTG (SEQ ID NO:1) cell wall sorting signal and other structural similarities to MSCRAMM® proteins having the LPXTG-anchored cell wall proteins. The MSCRAMM® proteins and immunogenic regions therein that are identified and isolated using the present invention may be used to generate antibodies useful in the diagnosis, treatment or prevention of Gram positive bacterial infections.

First Hit

L8: Entry 1 of 22

File: PGPB

Jul 22, 2004

PGPUB-DOCUMENT-NUMBER: 20040142348

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040142348 A1

TITLE: Proteins and polypeptides from coagulase-negative staphylococci

PUBLICATION-DATE: July 22, 2004

## INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
<u>Foster</u> , Timothy J.	Dublin	TX	IE	
McCrea, Kirk	Houston	TX	US	
<u>Hook</u> , Magnus A.O.	Houston	TX	US	
Davis, Stacey	Houston		US	
Nieidhin, Deirdre	Dublin		IE	
Hartford, Orla	Meath		IE	

APPL-NO: 10/ 689082 [PALM]

DATE FILED: October 21, 2003

## RELATED-US-APPL-DATA:

Application 10/689082 is a division-of US application 09/386962, filed August 31, 1999, US Patent No. 6635473

Application is a non-provisional-of-provisional application 60/117119, filed January 25, 1999,

Application is a non-provisional-of-provisional application 60/098443, filed August 31, 1998,

INT-CL: [07] C12 Q 1/68, C07 H 21/04, C07 K 14/31

US-CL-PUBLISHED: 435/006; 435/069.1, 435/252.3, 435/320.1, 530/350, 536/023.7

US-CL-CURRENT: 435/6; 435/252.3, 435/320.1, 435/69.1, 530/350, 536/23.7

REPRESENTATIVE-FIGURES: NONE

## ABSTRACT:

Proteins and polypeptides from coagulase-negative staphylococcal bacteria such as S. epidermidis, including proteins designated SdrF, SdrG and SdrH, and their effective fragments such as their respective A domains, are provided which are useful in the prevention and treatment of infection caused by coagulase-negative staphylococcal bacteria such as S. epidermidis. The SdrF, SdrG and SdrH proteins are cell-wall associated proteins that specifically bind host proteins and which each have a highly conserved motif of which the consensus sequence is TYTFTDYVD (SEQ ID NO: 16). The proteins and polypeptides may be useful in generating antibodies for the diagnosis and treatment of coagulase-negative staphylococcal infections.

## CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a divisional application of U.S. Appln. Ser. No. 09/386,962, filed Aug. 31, 1999, and claims the benefit of U.S. Provisional Applications Serial No. 60/117,119, filed Jan. 25, 1999, and Serial No. 60/098,443, filed Aug. 31, 1998.